

## WHAT IS CLAIMED IS:

1. A polynucleotide fragment comprising a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, wherein said polypeptide shares at least 70% homology with SEQ ID NOs:10, 14 or 44, as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin.

2. The polynucleotide fragment of claim 1, wherein said polynucleotide sequence includes nucleotides 63-1691 of SEQ ID NO:9.

3. The polynucleotide fragment of claim 1, wherein said polynucleotide sequence includes nucleotides 63-721 of SEQ ID NO:9.

4. The polynucleotide fragment of claim 1, wherein said polynucleotide is as set forth in SEQ ID NO:9.

5. The polynucleotide fragment of claim 1, wherein said polynucleotide sequence includes a segment of SEQ ID NO:9, said segment

6. The polynucleotide fragment of claim 1, wherein said polypeptide includes an amino acid sequence as set forth in SEQ ID NOs:10, 14 or 44.

7. The polynucleotide fragment of claim 1, wherein said polypeptide includes a segment of SEQ ID NOs:10, 14 or 44 said segment harbors said heparanase catalytic activity.

8. The polynucleotide fragment of claim 1, wherein said polynucleotide sequence is selected from the group consisting of double stranded DNA, single stranded DNA and RNA.

9. A polynucleotide sequence as set forth in SEQ ID NOs:9, 13, 42 or 43.

10. A polynucleotide sequence at least 70% homologous to SEQ ID NOs:9, 13, 42 or 43, as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin, wherein said polynucleotide sequence encodes a polypeptide having heparanase catalytic activity.

polypeptide having heparanase catalytic activity, wherein said polypeptide

shares at least 70% homology with SEQ ID NOs:10, 14 or 44, as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin.

12. The vector of claim 11, wherein said polynucleotide sequence includes nucleotides 63-1691 of SEQ ID NO:9.

13. The vector of claim 11, wherein said polynucleotide sequence includes nucleotides 63-721 of SEQ ID NO:9.

14. The vector of claim 11, wherein said polynucleotide sequence is as set forth in SEQ ID NO:9.

15. The vector of claim 11, wherein said polynucleotide sequence includes a segment of SEQ ID NO:9, said segment encodes said polypeptide having said heparanase catalytic activity.

16. The vector of claim 11, wherein said polypeptide includes an amino acid sequence as set forth in SEQ ID NOs:10, 14 or 44.

17. The vector of claim 11, wherein said polypeptide includes a segment of SEQ ID NOs:10, 14 or 44, said segment harbors said heparanase catalytic activity.

18. The vector of claim 11, wherein said polynucleotide sequence is selected from the group consisting of double stranded DNA, single stranded DNA and RNA.

19. The vector of claim 11, wherein said vector is a baculovirus vector.

20. A host cell comprising an exogenous polynucleotide fragment including a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, wherein said polypeptide shares at least 70% homology with SEQ ID NOs:10, 14 or 44, as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin.

21. The host cell of claim 20, wherein said polynucleotide sequence includes nucleotides 63-1691 of SEQ ID NO:9.

22. The host cell of claim 20, wherein said polynucleotide sequence includes nucleotides 63-721 of SEQ ID NO:9.

23. The host cell of claim 20, wherein said polynucleotide sequence is as set forth in SEQ ID NO:9.

24. The host cell of claim 20, wherein said polynucleotide sequence includes a segment of SEQ ID NO:9, said segment encodes said polypeptide having said heparanase catalytic activity.

25. The host cell of claim 20, wherein said polypeptide includes an amino acid sequence as set forth in SEQ ID NOs:10, 14 or 44.

26. The host cell of claim 20, wherein said polypeptide includes a segment of SEQ ID NOs:10, 14 or 44 said segment harbors said heparanase catalytic activity.

27. The host cell of claim 20, wherein said polynucleotide sequence is selected from the group consisting of double stranded DNA, single stranded DNA and RNA.

28. A host cell expressing a recombinant heparanase, wherein said recombinant heparanase shares at least 70% homology with SEQ ID NOs:10, 14 or 44, as determined using default parameter of a DNA sequence analysis software package developed by the Genetic Computer (Group (GCG) at the University of Wisconsin.

29. A heparanase overexpression system comprising a cell overexpressing heparanase catalytic activity, wherein said heparanase catalytic activity is effected by a heparanase sharing at least 70% homology with SEQ ID NOs:10, 14 or 44, as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin.

30. The host cell of claim 20, wherein said cell is an insect cell.